

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/003,919

DATE: 12/12/2001
 TIME: 14:26:26

Input Set : A:\RTS-0256 Sequence Listing.txt
 Output Set: N:\CRF3\12112001\I003919.raw

ENTERED

#2

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6 <110> APPLICANT: C. Frank Bennett
7   Susan M. Freier
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
11 <130> FILE REFERENCE: RTS-0256
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/003,919
C--> 13 <141> CURRENT FILING DATE: 2001-12-06
13 <160> NUMBER OF SEQ ID NOS: 87
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctcctcaggg                20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga                20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 5273
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (513)...(4079)
53 <400> SEQUENCE: 3
54 ctagggcacg gcatcccacg tgggtgtcag cacggccgca gaagaaccac ttctctggcc    60
55 caccocatgcc tgctaggcca tgcttcttca gaagtggcca caactctcct gacgtctcca    120
56 gagccggtca ttccaccacg ggggacttca gctgccactg gacacttcaa ttgtacgctg    180
57 cgaccagttg ccaggaagga gagggtctggc aagaaagccg cggcagccgt ggcagggtgt    240
58 atgggacggt ggacggccag ggcccccccc tctctctctt tctctctctc tctcttgcct    300
59 ggtttctgta atgaggaagt tctccgcagc tcagtttctt ttccctcact gagcgctga     360
60 aacagggaagt cagtcagtta agctggtggc agcagccgag gccaccaaga ggaacagggc    420
61 ggcagggtgc agtgaggagg cctccgctcc cctcgggtgt gtgtgggtcc tgggggtgcc    480
62 tgccggccca gccgaggagg cccaagccca cc atg gtc ccc tgc tgg aac cat     533
63                                     Met Val Pro Cys Trp Asn His
64                                     1                               5
65 ggc aac atc acc cgc tcc aag gcg gag gag ctg ctt tcc agg aca ggc      581
66 Gly Asn Ile Thr Arg Ser Lys Ala Glu Glu Leu Leu Ser Arg Thr Gly
67 10                               15                               20
68 aag gac ggg agc ttc ctc gtg cgt gcc agc gag tcc atc tcc cgg gca      629

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79 Lys Asp Gly Ser Phe Leu Val Arg Ala Ser Glu Ser Ile Ser Arg Ala
80      25              30              35
82 tac gcg ctc tgc gtg ctg tat cgg aat tgc gtt tac act tac aga att      677
83 Tyr Ala Leu Cys Val Leu Tyr Arg Asn Cys Val Tyr Thr Tyr Arg Ile
84 40      45              50              55
86 ctg ccc aat gaa gat gat aaa ttc act gtt cag gca tcc gaa ggc gtc      725
87 Leu Pro Asn Glu Asp Asp Lys Phe Thr Val Gln Ala Ser Glu Gly Val
88      60              65              70
90 tcc atg agg ttc ttc acc aag ctg gac cag ctc atc gag ttt tac aag      773
91 Ser Met Arg Phe Phe Thr Lys Leu Asp Gln Leu Ile Glu Phe Tyr Lys
92      75              80              85
94 aag gaa aac atg ggg ctg gtg acc cat ctg caa tac cct gtg ccg ctg      821
95 Lys Glu Asn Met Gly Leu Val Thr His Leu Gln Tyr Pro Val Pro Leu
96      90              95              100
98 gag gaa gag gac aca ggc gac gac cct gag gag gac aca gaa agt gtc      869
99 Glu Glu Glu Asp Thr Gly Asp Asp Pro Glu Glu Asp Thr Glu Ser Val
100      105              110              115
102 gtg tct cca ccc gag ctg ccc cca aga aac atc ccg ctg act gcc agc      917
103 Val Ser Pro Pro Glu Leu Pro Pro Arg Asn Ile Pro Leu Thr Ala Ser
104 120      125              130              135
106 tcc tgt gag gcc aag gag gtt cct ttt tca aac gag aat ccc cga gcg      965
107 Ser Cys Glu Ala Lys Glu Val Pro Phe Ser Asn Glu Asn Pro Arg Ala
108      140              145              150
110 acc gag acc agc cgg ccg agc ctc tcc gag aca ttg ttc cag cga ctg      1013
111 Thr Glu Thr Ser Arg Pro Ser Leu Ser Glu Thr Leu Phe Gln Arg Leu
112      155              160              165
114 caa agc atg gac acc agt ggg ctt cca gaa gag cat ctt aag gcc atc      1061
115 Gln Ser Met Asp Thr Ser Gly Leu Pro Glu Glu His Leu Lys Ala Ile
116      170              175              180
118 caa gat tat tta agc act cag ctc gcc cag gac tct gaa ttt gtg aag      1109
119 Gln Asp Tyr Leu Ser Thr Gln Leu Ala Gln Asp Ser Glu Phe Val Lys
120      185              190              195
122 aca ggg tcc agc agt ctt cct cac ctg aag aaa ctg acc aca ctg ctc      1157
123 Thr Gly Ser Ser Ser Leu Pro His Leu Lys Lys Leu Thr Thr Leu Leu
124 200      205              210              215
126 tgc aag gag ctc tat gga gaa gtc atc cgg acc ctc cca tcc ctg gag      1205
127 Cys Lys Glu Leu Tyr Gly Glu Val Ile Arg Thr Leu Pro Ser Leu Glu
128      220              225              230
130 tct ctg cag agg tta ttt gac cag cag ctc tcc ccg ggc ctc cgt cca      1253
131 Ser Leu Gln Arg Leu Phe Asp Gln Gln Leu Ser Pro Gly Leu Arg Pro
132      235              240              245
134 cgt cct cag gtt cct ggt gag gcc aat ccc atc aac atg gtg tcc aag      1301
135 Arg Pro Gln Val Pro Gly Glu Ala Asn Pro Ile Asn Met Val Ser Lys
136      250              255              260
138 ctc agc caa ctg aca agc ctg ttg tca tcc att gaa gac aag gtc aag      1349
139 Leu Ser Gln Leu Thr Ser Leu Leu Ser Ser Ile Glu Asp Lys Val Lys
140      265              270              275
142 gcc ttg ctg cac gag ggt cct gag tct ccg cac cgg ccc tcc ctt atc      1397
143 Ala Leu Leu His Glu Gly Pro Glu Ser Pro His Arg Pro Ser Leu Ile

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144	280		285		290		295	
146	cct cca gtc acc ttt gag gtc aag gca gag tct ctg ggg att cct cag	1445						
147	Pro Pro Val Thr Phe Glu Val Lys Ala Glu Ser Leu Gly Ile Pro Gln							
148			300		305		310	
150	aaa atg cag ctc aaa gtc gac gtt gag tct ggg aaa ctg atc att aag	1493						
151	Lys Met Gln Leu Lys Val Asp Val Glu Ser Gly Lys Leu Ile Ile Lys							
152			315		320		325	
154	aag tcc aag gat ggt tct gag gac aag ttc tac agc cac aag aaa atc	1541						
155	Lys Ser Lys Asp Gly Ser Glu Asp Lys Phe Tyr Ser His Lys Lys Ile							
156			330		335		340	
158	ctg cag ctc att aag tca cag aaa ttt ctg aat aag ttg gtg atc ttg	1589						
159	Leu Gln Leu Ile Lys Ser Gln Lys Phe Leu Asn Lys Leu Val Ile Leu							
160			345		350		355	
162	gtg gaa aca gag aag gag aag atc ctg cgg aag gaa tat gtt ttt gct	1637						
163	Val Glu Thr Glu Lys Glu Lys Ile Leu Arg Lys Glu Tyr Val Phe Ala							
164	360		365		370		375	
166	gac tcc aaa aag aga gaa ggc ttc tgc cag ctc ctg cag cag atg aag	1685						
167	Asp Ser Lys Lys Arg Glu Gly Phe Cys Gln Leu Leu Gln Gln Met Lys							
168			380		385		390	
170	aac aag cac tca gag cag ccg gag ccc gac atg atc acc atc ttc atc	1733						
171	Asn Lys His Ser Glu Gln Pro Glu Pro Asp Met Ile Thr Ile Phe Ile							
172			395		400		405	
174	ggc acc tgg aac atg ggt aac gcc ccc cct ccc aag aag atc acg tcc	1781						
175	Gly Thr Trp Asn Met Gly Asn Ala Pro Pro Pro Lys Lys Ile Thr Ser							
176			410		415		420	
178	tgg ttt ctc tcc aag ggg cag gga aag acg cgg gac gac tct gcg gac	1829						
179	Trp Phe Leu Ser Lys Gly Gln Gly Lys Thr Arg Asp Asp Ser Ala Asp							
180			425		430		435	
182	tac atc ccc cat gac att tac gtg atc ggc acc caa gag gac ccc ctg	1877						
183	Tyr Ile Pro His Asp Ile Tyr Val Ile Gly Thr Gln Glu Asp Pro Leu							
184	440		445		450		455	
186	agt gag aag gag tgg ctg gag atc ctc aaa cac tcc ctg caa gaa atc	1925						
187	Ser Glu Lys Glu Trp Leu Glu Ile Leu Lys His Ser Leu Gln Glu Ile							
188			460		465		470	
190	acc agt gtg act ttt aaa aca gtc gcc atc cac acg ctc tgg aac atc	1973						
191	Thr Ser Val Thr Phe Lys Thr Val Ala Ile His Thr Leu Trp Asn Ile							
192			475		480		485	
194	cgc atc gtg gtg ctg gcc aag cct gag cac gag aac cgg atc agc cac	2021						
195	Arg Ile Val Val Leu Ala Lys Pro Glu His Glu Asn Arg Ile Ser His							
196			490		495		500	
198	atc tgt act gac aac gtg aag aca ggc att gca aac aca ctg ggg aac	2069						
199	Ile Cys Thr Asp Asn Val Lys Thr Gly Ile Ala Asn Thr Leu Gly Asn							
200			505		510		515	
202	aag gga gcc gtg ggg gtg tcg ttc atg ttc aat gga acc tcc tta ggg	2117						
203	Lys Gly Ala Val Gly Val Ser Phe Met Phe Asn Gly Thr Ser Leu Gly							
204	520		525		530		535	
206	ttc gtc aac agc cac ttg act tca gga agt gaa aag aaa ctc agg cga	2165						
207	Phe Val Asn Ser His Leu Thr Ser Gly Ser Glu Lys Lys Leu Arg Arg							
208			540		545		550	

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210	aac	caa	aac	tat	atg	aac	att	ctc	cgg	ttc	ctg	gcc	ctg	ggc	gac	aag	2213
211	Asn	Gln	Asn	Tyr	Met	Asn	Ile	Leu	Arg	Phe	Leu	Ala	Leu	Gly	Asp	Lys	
212			555					560						565			
214	aag	ctg	agt	ccc	ttt	aac	atc	act	cac	cgc	ttc	acg	cac	ctc	ttc	tgg	2261
215	Lys	Leu	Ser	Pro	Phe	Asn	Ile	Thr	His	Arg	Phe	Thr	His	Leu	Phe	Trp	
216			570					575						580			
218	ttt	ggg	gat	ctt	aac	tac	cgt	gtg	gat	ctg	cct	acc	tgg	gag	gca	gaa	2309
219	Phe	Gly	Asp	Leu	Asn	Tyr	Arg	Val	Asp	Leu	Pro	Thr	Trp	Glu	Ala	Glu	
220			585					590						595			
222	acc	atc	atc	caa	aaa	atc	aag	cag	cag	cag	tac	gca	gac	ctc	ctg	tcc	2357
223	Thr	Ile	Ile	Gln	Lys	Ile	Lys	Gln	Gln	Gln	Tyr	Ala	Asp	Leu	Leu	Ser	
224	600					605					610					615	
226	cac	gac	cag	ctg	ctc	aca	gag	agg	agg	gag	cag	aag	gtc	ttc	cta	cac	2405
227	His	Asp	Gln	Leu	Leu	Thr	Glu	Arg	Arg	Glu	Gln	Lys	Val	Phe	Leu	His	
228					620					625						630	
230	ttc	gag	gag	gaa	gaa	atc	acg	ttt	gcc	cca	acc	tac	cgt	ttt	gag	aga	2453
231	Phe	Glu	Glu	Glu	Ile	Thr	Phe	Ala	Pro	Thr	Tyr	Arg	Phe	Glu	Arg		
232				635					640							645	
234	ctg	act	cgg	gac	aaa	tac	gcc	tac	acc	aag	cag	aaa	gcg	aca	ggg	atg	2501
235	Leu	Thr	Arg	Asp	Lys	Tyr	Ala	Tyr	Thr	Lys	Gln	Lys	Ala	Thr	Gly	Met	
236				650					655					660			
238	aag	tac	aac	ttg	cct	tcc	tgg	tgt	gac	cga	gtc	ctc	tgg	aag	tct	tat	2549
239	Lys	Tyr	Asn	Leu	Pro	Ser	Trp	Cys	Asp	Arg	Val	Leu	Trp	Lys	Ser	Tyr	
240			665					670						675			
242	ccc	ctg	gtg	cac	gtg	gtg	tgt	cag	tct	tat	ggc	agt	acc	agc	gac	atc	2597
243	Pro	Leu	Val	His	Val	Val	Cys	Gln	Ser	Tyr	Gly	Ser	Thr	Ser	Asp	Ile	
244	680					685					690					695	
246	atg	acg	agt	gac	cac	agc	cct	gtc	ttt	gcc	aca	ttt	gag	gca	gga	gtc	2645
247	Met	Thr	Ser	Asp	His	Ser	Pro	Val	Phe	Ala	Thr	Phe	Glu	Ala	Gly	Val	
248						700					705					710	
250	act	tcc	cag	ttt	gtc	tcc	aag	aac	ggg	ccc	ggg	act	gtt	gac	agc	caa	2693
251	Thr	Ser	Gln	Phe	Val	Ser	Lys	Asn	Gly	Pro	Gly	Thr	Val	Asp	Ser	Gln	
252				715					720							725	
254	gga	cag	att	gag	ttt	ctc	agg	tgc	tat	gcc	aca	ttg	aag	acc	aag	tcc	2741
255	Gly	Gln	Ile	Glu	Phe	Leu	Arg	Cys	Tyr	Ala	Thr	Leu	Lys	Thr	Lys	Ser	
256				730					735					740			
258	cag	acc	aaa	ttc	tac	ctg	gag	ttc	cac	tcg	agc	tgc	ttg	gag	agt	ttt	2789
259	Gln	Thr	Lys	Phe	Tyr	Leu	Glu	Phe	His	Ser	Ser	Cys	Leu	Glu	Ser	Phe	
260				745					750					755			
262	gtc	aag	agt	cag	gaa	gga	gaa	aat	gaa	gaa	gga	agt	gag	ggg	gag	ctg	2837
263	Val	Lys	Ser	Gln	Glu	Gly	Glu	Asn	Glu	Glu	Gly	Ser	Glu	Gly	Glu	Leu	
264	760					765					770					775	
266	gtg	gtg	aag	ttt	ggg	gag	act	ctt	cca	aag	ctg	aag	ccc	att	atc	tct	2885
267	Val	Val	Lys	Phe	Gly	Glu	Thr	Leu	Pro	Lys	Leu	Lys	Pro	Ile	Ile	Ser	
268					780						785					790	
270	gac	cct	gag	tac	ctg	cta	gac	cag	cac	atc	ctc	atc	agc	atc	aag	tcc	2933
271	Asp	Pro	Glu	Tyr	Leu	Leu	Asp	Gln	His	Ile	Leu	Ile	Ser	Ile	Lys	Ser	
272					795					800						805	
274	tct	gac	agc	gac	gaa	tcc	tat	ggc	gag	ggc	tgc	att	gcc	ctt	cgg	tta	2981

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275 Ser Asp Ser Asp Glu Ser Tyr Gly Glu Gly Cys Ile Ala Leu Arg Leu
276      810      815      820
278 gag gcc aca gaa acg cag ctg ccc atc tac acg cct ctc acc cac cat      3029
279 Glu Ala Thr Glu Thr Gln Leu Pro Ile Tyr Thr Pro Leu Thr His His
280      825      830      835
282 ggg gag ttg aca ggc cac ttc cag ggg gag atc aag ctg cag acc tct      3077
283 Gly Glu Leu Thr Gly His Phe Gln Gly Glu Ile Lys Leu Gln Thr Ser
284 840      845      850      855
286 cag ggc aag acg agg gag aag ctc tat gac ttt gtg aag acg gag cgt      3125
287 Gln Gly Lys Thr Arg Glu Lys Leu Tyr Asp Phe Val Lys Thr Glu Arg
288      860      865      870
290 gat gaa tcc agt ggg cca aag acc ctg aag agc ctc acc agc cac gac      3173
291 Asp Glu Ser Ser Gly Pro Lys Thr Leu Lys Ser Leu Thr Ser His Asp
292      875      880      885
294 ccc atg aag cag tgg gaa gtc act agc agg gcc cct ccg tgc agt ggc      3221
295 Pro Met Lys Gln Trp Glu Val Thr Ser Arg Ala Pro Pro Cys Ser Gly
296      890      895      900
298 tcc agc atc act gaa atc atc aac ccc aac tac atg gga gtg ggg ccc      3269
299 Ser Ser Ile Thr Glu Ile Ile Asn Pro Asn Tyr Met Gly Val Gly Pro
300      905      910      915
302 ttt ggg cca cca atg ccc ctg cac gtg aag cag acc ttg tcc cct gac      3317
303 Phe Gly Pro Pro Met Pro Leu His Val Lys Gln Thr Leu Ser Pro Asp
304 920      925      930      935
306 cag cag ccc aca gcc tgg agc tac gac cag ccg ccc aag gac tcc ccg      3365
307 Gln Gln Pro Thr Ala Trp Ser Tyr Asp Gln Pro Pro Lys Asp Ser Pro
308      940      945      950
310 ctg ggg ccc tgc agg gga gaa agt cct ccg aca cct ccc ggc cag ccg      3413
311 Leu Gly Pro Cys Arg Gly Glu Ser Pro Pro Thr Pro Pro Gly Gln Pro
312      955      960      965
314 ccc ata tca ccc aag aag ttt tta ccc tca aca gca aac cgg ggt ctc      3461
315 Pro Ile Ser Pro Lys Lys Phe Leu Pro Ser Thr Ala Asn Arg Gly Leu
316      970      975      980
318 cct ccc agg aca cag gag tca agg ccc agt gac ctg ggg aag aac gca      3509
319 Pro Pro Arg Thr Gln Glu Ser Arg Pro Ser Asp Leu Gly Lys Asn Ala
320      985      990      995
322 ggg gag acg ctg cct cag gag gac ctg ccg ctg acg aag ccc gag atg      3557
323 Gly Asp Thr Leu Pro Gln Glu Asp Leu Pro Leu Thr Lys Pro Glu Met
324 1000      1005      1010      1015
326 ttt gag aac ccc ctg tat ggg tcc ctg agt tcc ttc cct aag cct gct      3605
327 Phe Glu Asn Pro Leu Tyr Gly Ser Leu Ser Ser Phe Pro Lys Pro Ala
328      1020      1025      1030
330 ccc agg aag gac cag gaa tcc ccc aaa atg ccg cgg aag gaa ccc ccg      3653
331 Pro Arg Lys Asp Gln Glu Ser Pro Lys Met Pro Arg Lys Glu Pro Pro
332      1035      1040      1045
334 ccc tgc ccg gaa ccc ggc atc ttg tgc ccc agc atc gtg ctc acc aaa      3701
335 Pro Cys Pro Glu Pro Gly Ile Leu Ser Pro Ser Ile Val Leu Thr Lys
336      1050      1055      1060
338 gcc cag gag gct gat cgc ggc gag ggg ccc ggc aag cag gtg ccc gcg      3749
339 Ala Gln Glu Ala Asp Arg Gly Glu Gly Pro Gly Lys Gln Val Pro Ala

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date